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FILE 'HOME' ENTERED AT 18:40:56 ON 10 FEB 2006

=> file .nash
=> s fibroblast activat? protein or fap
L1        2153 FILE MEDLINE
L2        1597 FILE CAPLUS
L3        2284 FILE SCISEARCH
L4         399 FILE LIFESCI
L5        1905 FILE BIOSIS
L6        1876 FILE EMBASE

TOTAL FOR ALL FILES
L7       10214 FIBROBLAST ACTIVAT? PROTEIN OR FAP

=> s fibroblast activat? protein or fap or seprase
TOTAL FOR ALL FILES
L14      10319 FIBROBLAST ACTIVAT? PROTEIN OR FAP OR SEPRASE

=> s fibroblast activat? protein or seprase
TOTAL FOR ALL FILES
L21        591 FIBROBLAST ACTIVAT? PROTEIN OR SEPRASE

=> s l21 and crystal?
TOTAL FOR ALL FILES
L28         18 L21 AND CRYSTAL?

=> s l28 not 2003-2006/py
TOTAL FOR ALL FILES
L35          0 L28 NOT 2003-2006/PY

=> dup rem l28
PROCESSING COMPLETED FOR L28
L36          10 DUP REM L28 (8 DUPLICATES REMOVED)

=> d ibib abs 1-10

L36  ANSWER 1 OF 10  CAPLUS  COPYRIGHT 2006 ACS on STN
ACCESSION NUMBER:         2005:409763  CAPLUS Full-text
DOCUMENT NUMBER:          142:459625
TITLE:                    Cell adhesion matrix mimicking a metastatic,
                          cardiovascular or placental environment for diagnosis
                          of diseases
INVENTOR(S):              Chen, Wen-Tien; Chen, Lee; Chen, Che
PATENT ASSIGNEE(S):       Vitatex, Inc., USA
SOURCE:                   PCT Int. Appl., 92 pp.
                          CODEN: PIXXD2
DOCUMENT TYPE:            Patent
LANGUAGE:                 English
FAMILY ACC. NUM. COUNT:   4
PATENT INFORMATION:

     PATENT NO.          KIND   DATE        APPLICATION NO.        DATE
     ---------------     ----   --------    --------------------   --------
     WO 2005043121        A2    20050512    WO 2004-US36177        20041030
         W:  AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BW, BY, BZ, CA, CH,
             CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, EG, ES, FI, GB, GD,
             GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC,
             LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NA, NI,
             NO, NZ, OM, PG, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, SY,
             TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW
        RW:  BW, GH, GM, KE, LS, MW, MZ, NA, SD, SL, SZ, TZ, UG, ZM, ZW, AM,
             AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, BG, CH, CY, CZ, DE, DK,
             EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PL, PT, RO, SE,
             SI, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE,
             SN, TD, TG
PRIORITY APPLN. INFO.:                      US 2003-516571P      P  20031031
AB      Methods and devices for isolating and diagnosing disease with a cell adhesion matrix
        system, mimicking a metastatic, cardiovascular or placental environment, are disclosed.
        The cell adhesion matrix facilitates the enrichment of target cells such as metastatic
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tumor cells, fetal cells and endothelial progenitor cells from a fluid sample such as blood for diagnostic and therapeutic application s in treating patients afflicted with disease, such as cancerous, cardiovascular and fetal diseases, as well as for research applications in mol. anal. of metastatic, and cardiovascular and fetal diseases. Blood test prototypes and methods for the cell enrichment and detection of circulating tumor and endothelial cells using multiplex mol. anal. are described herein. In addition, methods and compns. for determining host immunity to tumor in subjects with risk of cancer progression and methods for isolating an enriched fraction of fetal cells from pregnant females for prenatal diagnosis are also described herein.

L36 ANSWER 2 OF 10 CAPLUS COPYRIGHT 2006 ACS on STN
ACCESSION NUMBER: 2005:1020555 CAPLUS Full-text
DOCUMENT NUMBER: 143:320266
TITLE: Genes with differential expression profile between human dental pulp stem cells and mesenchymal stem cells and use for regenerating tooth germ
INVENTOR(S): Ueda, Minoru; Yamada, Yoichi
PATENT ASSIGNEE(S): Hitachi Medical Corp., Japan
SOURCE: Jpn. Kokai Tokkyo Koho, 246 pp.
CODEN: JKXXAF
DOCUMENT TYPE: Patent
LANGUAGE: Japanese
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
	JP 2005253442	A2	20050922	JP 2004-111582	20040309
PRIORITY APPLN. INFO.:				JP 2004-111582	20040309

AB The present invention relates to a group of genes whose expression profile are different between human dental pulp stem cells and mesenchymal stem cells, as well as a method for regenerating tooth germ using these genes. According to the present invention, the gene expression profiles and cluster anal. between human dental pulp stem cells (hDPSCs) and mesenchymal stem cells (hMSCs) as representative populations of odontoprogenitor and osteoprogenitor cell were revealed, and a group of genes whose expression profile are different between human dental pulp stem cells and mesenchymal stem cells was identified. By utilizing the groups of the genes of the present invention together with the dental pulp stem cells and mesenchymal stem cells, hard tissue such as tooth germ, dental pulp, dentin or bone can be regenerated. The present inventors investigated the gene expression profiles and cluster anal. between human dental pulp stem cells (hDPSCs) and mesenchymal stem cells (hMSCs) as representative populations of odontoprogenitor and osteoprogenitor cells, resp. At first, the present inventors confirmed the differential expression of Alkaline phosphatase (ALP) activity, Dentin matrix protein 1 (DMP 1), Dentin phosphosialoprotein (DSPP) using by real time reverse-transcriptase polymerase chain reaction (RT-PCR) in total RNA from primary cultures. The number of genes in hDPSCs(I) that were up-regulated by 2>-fold, compared to hMSCs, was 614 (Table, IV). On the other band, the number of genes down regulated by <2-fold in hDPSCs (I) was 296 (Table III, IV).

L36 ANSWER 3 OF 10 MEDLINE on STN DUPLICATE 1
ACCESSION NUMBER: 2005256428 MEDLINE Full-text
DOCUMENT NUMBER: PubMed ID: 15809306
TITLE: Structural and kinetic analysis of the substrate specificity of human fibroblast activation protein alpha.
AUTHOR: Aertgeerts Kathleen; Levin Irena; Shi Lihong; Snell Gyorgy P; Jennings Andy; Prasad G Sridhar; Zhang Yanming; Kraus Michelle L; Salakian Shant; Sridhar Vandana; Wijnands Robert; Tennant Mike G
CORPORATE SOURCE: Takeda San Diego, Inc., California 92121, USA.. kaertgeerts@takedasd.com
SOURCE: Journal of biological chemistry, (2005 May 20) 280 (20) 19441-4. Electronic Publication: 2005-04-04.
Journal code: 2985121R. ISSN: 0021-9258.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: PDB-1Z68
ENTRY MONTH: 200507

ENTRY DATE: Entered STN: 20050518
Last Updated on STN: 20050709
Entered Medline: 20050708

AB Fibroblast activation protein alpha (FAPalpha) is highly expressed in epithelial cancers and has been implicated in extracellular matrix remodeling, tumor growth, and metastasis. We present the first high resolution structure for the apoenzyme as well as kinetic data toward small dipeptide substrates. FAPalpha exhibits a dipeptidyl peptidase IV (DPPIV)-like fold, featuring an alpha/beta-hydrolase domain and an eight-bladed beta-propeller domain. Known DPPIV dipeptides are cleaved by FAPalpha with an approximately 100-fold decrease in catalytic efficiency compared with DPPIV. Moreover, FAPalpha, but not DPPIV, possesses endopeptidase activity toward N-terminal benzyloxycarbonyl (Z)-blocked peptides. Comparison of the crystal structures of FAPalpha and DPPIV revealed one major difference in the vicinity of the Glu motif (Glu(203)-Glu(204) for FAPalpha; Glu(205)-Glu(206) for DPPIV) within the active site of the enzyme. Ala(657) in FAPalpha, instead of Asp(663) as in DP-PIV, reduces the acidity in this pocket, and this change could explain the lower affinity for N-terminal amines by FAPalpha. This hypothesis was tested by kinetic analysis of the mutant FAPalpha/A657D, which shows on average an approximately 60-fold increase in the catalytic efficiency, as measured by k(cat)/K(m), for the cleavage of dipeptide substrates. Furthermore, the catalytic efficiency of the mutant is reduced by approximately 350-fold for cleavage of Z-Gly-Pro-7-amino-4-methylcoumarin. Our data provide a clear understanding of the molecular determinants responsible for the substrate specificity and endopeptidase activity of FAPalpha.

L36 ANSWER 4 OF 10 SCISEARCH COPYRIGHT (c) 2006 The Thomson Corporation on STN
ACCESSION NUMBER: 2005:341157 SCISEARCH Full-text
THE GENUINE ARTICLE: 908YB
TITLE: The therapeutic potential of inhibitors of dipeptidyl peptidase IV (DPP IV) and related proline-specific dipeptidyl aminopeptidases
AUTHOR: Augustyns K (Reprint); Van der Veken P; Senten K; Haemers A
CORPORATE SOURCE: Univ Antwerp, Dept Med Chem, Univ Plein 1, B-2610 Antwerp, Belgium (Reprint); Univ Antwerp, Dept Med Chem, B-2610 Antwerp, Belgium
Koen.Augustyns@ua.ac.be
COUNTRY OF AUTHOR: Belgium
SOURCE: CURRENT MEDICINAL CHEMISTRY, (2005) Vol. 12, No. 8, pp. 971-998.
ISSN: 0929-8673.
PUBLISHER: BENTHAM SCIENCE PUBL LTD, EXECUTIVE STE Y26, PO BOX 7917, SAIF ZONE, 1200 BR SHARJAH, U ARAB EMIRATES.
DOCUMENT TYPE: General Review; Journal
LANGUAGE: English
REFERENCE COUNT: 274
ENTRY DATE: Entered STN: 7 Apr 2005
Last Updated on STN: 7 Apr 2005
ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

AB In this review the structural and functional aspects of dipeptidyl peptidase IV (DPP IV) will be described, and the therapeutic potential of DPP IV inhibitors will be highlighted. DPP IV will be situated in clan SC, a group of serine proteases that contains several proline specific peptidases. Structural aspects of DPP IV and its interaction with different types of inhibitors are recently revealed by the publication of several crystal structures. Especially the design and development of new DPP IV inhibitors based on the three-dimensional structure, substrate specificity and catalytic mechanism will be discussed. In the last years there was an important development of new pyrrolidine-2-nitriles with very promising therapeutic properties for the treatment of type 2 diabetes. The role of DPP IV in peptide metabolism of members of the PACAP/glucagon peptide family, neuropeptides and chemokines has been thoroughly investigated during recent years. This is directly related to the promising therapeutic potential of DPP IV inhibitors in the treatment of type 2 diabetes and in the treatment of immunological disorders. Several inhibitors are currently under investigation in clinical trials for the treatment of type 2 diabetes and represent a new class of drugs for the treatment of this disease.

L36 ANSWER 5 OF 10 MEDLINE on STN DUPLICATE 2
ACCESSION NUMBER: 2005135394 MEDLINE Full-text
DOCUMENT NUMBER: PubMed ID: 15584901

TITLE: Dipeptidyl peptidase IV and related enzymes in cell biology and liver disorders.
AUTHOR: Gorrell Mark D
CORPORATE SOURCE: A.W. Morrow Gastroenterology and Liver Centre at Royal Prince Alfred Hospital, Centenary Institute of Cancer Medicine and Cell Biology and Discipline of Medicine, The University of Sydney, Sydney, New South Wales, Australia.. M.Gorrell@centenary.usyd.edu.au
SOURCE: Clinical science (London, England : 1979), (2005 Apr) 108 (4) 277-92. Ref: 137
Journal code: 7905731. ISSN: 0143-5221.
PUB. COUNTRY: England: United Kingdom
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
General Review; (REVIEW)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200505
ENTRY DATE: Entered STN: 20050316
Last Updated on STN: 20050504
Entered Medline: 20050503

AB DP (dipeptidyl peptidase) IV is the archetypal member of its six-member gene family. Four members of this family, DPIV, FAP (fibroblast activation protein), DP8 and DP9, have a rare substrate specificity, hydrolysis of a prolyl bond two residues from the N-terminus. The ubiquitous DPIV glycoprotein has proved interesting in the fields of immunology, endocrinology, haematology and endothelial cell and cancer biology and DPIV has become a novel target for Type II diabetes therapy. The crystal structure shows that the soluble form of DPIV comprises two domains, an alpha/beta-hydrolase domain and an eight-blade beta-propeller domain. The propeller domain contains the ADA (adenosine deaminase) binding site, a dimerization site, antibody epitopes and two openings for substrate access to the internal active site. FAP is structurally very similar to DPIV, but FAP protein expression is largely confined to diseased and damaged tissue, notably the tissue remodelling interface in chronically injured liver. DPIV has a variety of peptide substrates, the best studied being GLP-1 (glucagon-like peptide-1), NPY (neuropeptide Y) and CXCL12. The DPIV family has roles in bone marrow mobilization. The functional interactions of DPIV and FAP with extracellular matrix confer roles for these proteins in cancer biology. DP8 and DP9 are widely distributed and indirectly implicated in immune function. The DPL (DP-like) glycoproteins that lack peptidase activity, DPL1 and DPL2, are brain-expressed potassium channel modulators. Thus the six members of the DPIV gene family exhibit diverse biological roles.

L36 ANSWER 6 OF 10 CAPLUS COPYRIGHT 2006 ACS on STN
ACCESSION NUMBER: 2005:1199755 CAPLUS Full-text
TITLE: Diverse functions in a conserved structure: the dipeptidyl peptidase IV gene family
AUTHOR(S): Gorrell, Mark D.; Yu, Denise M. T.
CORPORATE SOURCE: A. W. Morrow Gastroenterology and Liver Centre at Royal Prince Alfred Hospital, Centenary Institute of Cancer Medicine and Cell Biology and Discipline of Medicine, The University of Sydney, Sydney, Australia
SOURCE: Trends in Protein Research (2005), 1-78. Editor(s): Robinson, John W. Nova Science Publishers, Inc.: Hauppauge, N. Y.
CODEN: 69HNTS; ISBN: 1-59454-153-1
DOCUMENT TYPE: Conference
LANGUAGE: English

AB Dipeptidyl Peptidase IV (DP-IV) is the archetypal member of its six-member gene family. Four members of this family, DP-IV, fibroblast activation protein (FAP), DP8 and DP9 have a rare enzyme activity, hydrolysis of a prolyl bond two residues from the N terminus. The ubiquitous DP-IV glycoprotein has proved interesting in the fields of metabolism, immunol., endocrinol. and endothelial cell and cancer biol. DP-IV substrates include neuropeptide Y, nine chemokines, glucose-dependent insulinotropic peptide and glucagon-like peptide. In addition, DP-IV helps protect T cells from adenosine toxicity by binding adenosine deaminase (ADA) to the cell surface. FAP exhibits a gelatinase activity. The structure of DP-IV has been sought to facilitate development of inhibitors for use in diabetes type 2 therapy. Six independent groups have reported crystal structures of DP-IV. The soluble form of DP-IV comprises two domains; an α/β-hydrolase domain contributed by both N- and C- terminal sequences and an 8-blade β-propeller domain. The propeller domain contains the ADA binding site, a dimerization site, antibody epitopes and openings for potential substrate access to the internal active site. Biochem. data on point mutations fit well with the structure. A sequence motif unique to the DP-IV gene family

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         contains a pair of glutamates that are essential for catalytic activity in DP-IV and DP8.
         The DP-IV structure shows that these glutamates anchor the amino terminus of substrates.
         FAP is structurally very similar to DP-IV but FAP protein expression is confined to
         diseased and damaged tissue whereas DP-IV is ubiquitous.  DP8 and DP9 are widely
         distributed.  The two non-enzyme members of this gene family, DP-like (DPL) 1 and DPL2,
         are primarily brain expressed.  Recent studies have provided new insights into the
         mechanisms of action of DP-IV in T cell proliferation.  Consideration of the DP-IV crystal
         structure has provided a greater understanding of its peptidase activity and interactions
         with ligands.
REFERENCE COUNT:          372    THERE ARE 372 CITED REFERENCES AVAILABLE FOR
                                 THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE
                                 FORMAT

L36  ANSWER 7 OF 10  CAPLUS  COPYRIGHT 2006 ACS on STN
ACCESSION NUMBER:         2004:449883  CAPLUS Full-text
DOCUMENT NUMBER:          140:402911
TITLE:                    Binary prediction tree modeling with many predictors
                          and its uses in clinical and genomic applications
INVENTOR(S):              Nevins, Joseph R.; West, Mike; Huang, Andrew T.
PATENT ASSIGNEE(S):       Duke University, USA
SOURCE:                   PCT Int. Appl., 886 pp.
                          CODEN: PIXXD2
DOCUMENT TYPE:            Patent
LANGUAGE:                 English
FAMILY ACC. NUM. COUNT:   5
PATENT INFORMATION:

     PATENT NO.          KIND   DATE        APPLICATION NO.        DATE
     ---------------     ----   --------    -------------------    --------
     WO 2004038376        A2    20040506    WO 2003-XA33946        20031024
         W:  AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN,
             CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, EG, ES, FI, GB, GD, GE,
             GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK,
             LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NI, NO, NZ,
             OM, PG, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, SY, TJ, TM,
             TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW, AM, AZ,
             BY, KG, KZ, MD
         RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, BG,
             CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC,
             NL, PT, RO, SE, SI, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ,
             GW, ML, MR, NE, SN, TD, TG
     WO 2004038376        A2    20040506    WO 2003-US33946        20031024
     WO 2004038376        A3    20040826
         W:  AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN,
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             GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK,
             LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NI, NO, NZ,
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             KG, KZ, MD, RU, TJ, TM, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES,
             FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PT, RO, SE, SI, SK, TR,
             BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG
PRIORITY APPLN. INFO.:                      US 2002-420729P     P  20021024
                                            US 2002-421062P     P  20021025
                                            US 2002-421102P     P  20021025
                                            US 2002-424701P     P  20021108
                                            US 2002-424715P     P  20021108
                                            US 2002-424718P     P  20021108
                                            US 2002-425256P     P  20021112
                                            US 2003-448461P     P  20030221
                                            US 2003-448462P     P  20030221
                                            US 2003-457877P     P  20030327
                                            US 2003-458373P     P  20030331
                                            WO 2003-US33946     A  20031024
AB       The statistical anal. described and claimed is a predictive statistical tree model that
         overcomes several problems observed in prior statistical models and regression analyses,
         while ensuring greater accuracy and predictive capabilities.  Although the claimed use of
         the predictive statistical tree model described herein is directed to the prediction of a
         disease in individuals, the claimed model can be used for a variety of applications
         including the prediction of disease states, susceptibility of disease states or any other
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biol. state of interest, as well as other applicable non-biol. states of interest. This model first screens genes to reduce noise, applies kmeans correlation-based clustering targeting a large number of clusters, and then uses singular value decompns. (SVD) to extract the single dominant factor (principal component) from each cluster. This generates a statistically significant number of cluster-derived singular factors, that are referred to as metagenes, that characterize multiple patterns of expression of the genes across samples. The strategy aims to extract multiple such patterns while reducing dimension and smoothing out gene-specific noise through the aggregation within clusters. Formal predictive anal. then uses these metagenes in a Bayesian classification tree anal. This generates multiple recursive partitions of the sample into subgroups (the 'leaves' of the classification tree), and assocs. Bayesian predictive probabilities of outcomes with each subgroup. Overall predictions for an individual sample are then generated by averaging predictions, with appropriate wts., across many such tree models. The model includes the use of iterative out-of-sample, cross-validation predictions leaving each sample out of the data set one at a time, refitting the model from the remaining samples and using it to predict the hold-out case. This rigorously tests the predictive value of a model and mirrors the real-world prognostic context where prediction of new cases as they arise is the major goal.

L36 ANSWER 8 OF 10 SCISEARCH COPYRIGHT (c) 2006 The Thomson Corporation on STN
ACCESSION NUMBER: 2004:63829 SCISEARCH Full-text
THE GENUINE ARTICLE: 757XX
TITLE: N-linked glycosylation of dipeptidyl peptidase IV (CD26): Effects on enzyme activity, homodimer formation, and adenosine deaminase binding
AUTHOR: Aertgeerts K (Reprint); Ye S; Shi L H; Prasad S G; Witmer D; Chi E; Sang B C; Wijnands R A; Webb D R; Swanson R V
CORPORATE SOURCE: Syrrx Inc, 10410 Sci Ctr Dr, San Diego, CA 92121 USA (Reprint); Syrrx Inc, San Diego, CA 92121 USA
COUNTRY OF AUTHOR: USA
SOURCE: PROTEIN SCIENCE, (JAN 2004) Vol. 13, No. 1, pp. 145-154. ISSN: 0961-8368.
PUBLISHER: COLD SPRING HARBOR LAB PRESS, PUBLICATIONS DEPT, 500 SUNNYSIDE BLVD, WOODBURY, NY 11797-2924 USA.
DOCUMENT TYPE: Article; Journal
LANGUAGE: English
REFERENCE COUNT: 32
ENTRY DATE: Entered STN: 23 Jan 2004
Last Updated on STN: 23 Jan 2004
ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

AB The type II transmembrane serine protease dipeptidyl peptidase IV (DPPIV), also known as CD26 or adenosine deaminase binding protein, is a major regulator of various physiological processes, including immune, inflammatory, nervous, and endocrine functions. It has been generally accepted that glycosylation of DPPIV and of other transmembrane dipeptidyl peptidases is a prerequisite for enzyme activity and correct protein folding. Crystallographic studies on DPPIV reveal clear N-linked glycosylation of nine Asn residues in DPPIV. However, the importance of each glycosylation site on physiologically relevant reactions such as dipeptide cleavage, dimer formation, and adenosine deaminase (ADA) binding remains obscure. Individual Asn-->Ala point mutants were introduced at the nine glycosylation sites in the extracellular domain of DPPIV (residues 39-766). Crystallographic and biochemical data demonstrate that N-linked glycosylation of DPPIV does not contribute significantly to its peptidase activity. The kinetic parameters of dipeptidyl peptidase cleavage of wild-type DPPIV and the N-glycosylation site mutants were determined by using Ala-Pro-AFC and Gly-Pro-pNA as substrates and varied by <50%. DPPIV is active as a homodimer. Size-exclusion chromatographic analysis showed that the glycosylation site mutants do not affect dimerization. ADA binds to the highly glycosylated beta-propeller domain of DPPIV, but the impact of glycosylation on binding had not previously been determined. Our studies indicate that glycosylation of DPPIV is not required for ADA binding. Taken together, these data indicate that in contrast to the generally accepted view, glycosylation of DPPIV is not a prerequisite for catalysis, dimerization, or ADA binding.

L36 ANSWER 9 OF 10 CAPLUS COPYRIGHT 2006 ACS on STN
ACCESSION NUMBER: 2003:942764 CAPLUS Full-text
DOCUMENT NUMBER: 140:3792
TITLE: Genes expressed in atherosclerotic tissue and their

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                         use in diagnosis and pharmacogenetics
INVENTOR(S):             Nevins, Joseph; West, Mike; Goldschmidt, Pascal
PATENT ASSIGNEE(S):      Duke University, USA
SOURCE:                  PCT Int. Appl., 408 pp.
                         CODEN: PIXXD2
DOCUMENT TYPE:           Patent
LANGUAGE:                English
FAMILY ACC. NUM. COUNT:  3
PATENT INFORMATION:

     PATENT NO.          KIND  DATE        APPLICATION NO.        DATE
     ---------------     ----  --------    --------------------   --------
     WO 2003091391        A2   20031106    WO 2002-XA38221        20021112
         W:  AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ,
             DE, DK, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IS, JP,
             KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN,
             MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM,
             TR, TT, UA, UG, UZ, VN, YU, ZA, ZW
         RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, BG,
             CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL,
             PT, SE, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR,
             NE, SN, TD, TG
     WO 2003091391        A2   20031106    WO 2002-US38221        20021112
         W:  AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ,
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             KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN,
             MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM,
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             FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, SK, TR, BF, BJ, CF,
             CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG
PRIORITY APPLN. INFO.:                      US 2002-374547P     P  20020423
                                            US 2002-420784P     P  20021024
                                            US 2002-421043P     P  20021025
                                            US 2002-424680P     P  20021108
                                            WO 2002-US38221     A  20021112
AB     Genes whose expression is correlated with an determinant of an atherosclerotic phenotype
       are provided.  Also provided are methods of using the subject atherosclerotic determinant
       genes in diagnosis and treatment methods, as well as drug screening methods.  In addition,
       reagents and kits thereof that find use in practicing the subject methods are provided.
       Also provided are methods of determining whether a gene is correlated with a disease
       phenotype, where correlation is determined using a Bayesian anal.


L36  ANSWER 10 OF 10  SCISEARCH  COPYRIGHT (c) 2006 The Thomson Corporation  on
     STN
ACCESSION NUMBER:    2003:394573  SCISEARCH Full-text
THE GENUINE ARTICLE: 673ZY
TITLE:               The crystal structure of dipeptidyl peptidase
                     IV(CD26) reveals its functional regulation and enzymatic
                     mechanism
AUTHOR:              Engel M; Hoffmann T; Wagner L; Wermann M; Heiser U;
                     Kiefersauer R; Huber R; Bode W; Demuth H U (Reprint);
                     Brandstetter H
CORPORATE SOURCE:    Proteros Biostruct GmbH, Klopferspitz 19, D-82152
                     Martinsried, Germany (Reprint); Proteros Biostruct GmbH,
                     D-82152 Martinsried, Germany; Probiodrug AG, Biozentrum,
                     D-06120 Halle Saale, Germany; Max Planck Inst Biochem, Abt
                     Strukturforsch, D-82152 Martinsried, Germany
COUNTRY OF AUTHOR:   Germany
SOURCE:              PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE
                     UNITED STATES OF AMERICA, (29 APR 2003) Vol. 100, No. 9,
                     pp. 5063-5068.
                     ISSN: 0027-8424.
PUBLISHER:           NATL ACAD SCIENCES, 2101 CONSTITUTION AVE NW, WASHINGTON,
                     DC 20418 USA.
DOCUMENT TYPE:       Article; Journal
LANGUAGE:            English
REFERENCE COUNT:     58
ENTRY DATE:          Entered STN: 23 May 2003
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                   Last Updated on STN: 23 May 2003
                  *ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS*
AB            The membrane-bound glycoprotein dipeptidyl peptidase IV (DP IV, CD26) is a unique
              multifunctional protein, acting as receptor, binding and proteolytic molecule.  We
              have determined the sequence and 1.8 A crystal structure of native DP IV prepared
              from porcine kidney. The crystal structure reveals a 2-2-2 symmetric tetrameric
              assembly which depends on the natively glycosylated beta-propeller blade IV.  The
              crystal structure indicates that tetramerization of DP IV is a key mechanism to
              regulate its interaction with other components. Each subunit comprises two
              structural domains, the N-terminal eight-bladed beta-propeller with open Velcro
              topology and the C-terminal alpha/beta-hydrolase domain.  Analogy with the
              structurally related POP and tricorn protease suggests that substrates access the
              buried active site through the p-propeller tunnel while products leave the active
              site through a separate side exit.  A dipeptide mimicking inhibitor complexed to
              the active site discloses key determinants for substrate recognition, including a
              Glu-Glu motif that distinguishes DIP IV as an aminopeptidase and an oxyanion trap
              that binds and activates the P-2-carbonyl oxygen necessary for efficient
              postproline cleavage.  We discuss active and nonactive site-directed inhibition
              strategies of this pharmaceutical target protein.



=> s l21 and x-ray
L37           1 FILE MEDLINE
L38           5 FILE CAPLUS
L39           0 FILE SCISEARCH
L40           0 FILE LIFESCI
L41           0 FILE BIOSIS
L42           0 FILE EMBASE

TOTAL FOR ALL FILES
L43           6 L21 AND X-RAY

=> dup rem l43
PROCESSING COMPLETED FOR L43
L44            4 DUP REM L43 (2 DUPLICATES REMOVED)

=> d ibib abs

L44  ANSWER 1 OF 4  CAPLUS  COPYRIGHT 2006 ACS on STN  DUPLICATE 1
ACCESSION NUMBER:         2005:172213  CAPLUS Full-text
DOCUMENT NUMBER:          142:259426
TITLE:                    Gene expression profiles and biomarkers for the
                          detection of asthma-related and other disease-related
                          gene transcripts in blood
INVENTOR(S):              Liew, Choong-Chin
PATENT ASSIGNEE(S):       Chondrogene Limited, Can.
SOURCE:                   U.S. Pat. Appl. Publ., 156 pp., Cont.-in-part of U.S.
                          Ser. No. 802,875.
                          CODEN: USXXCO
DOCUMENT TYPE:            Patent
LANGUAGE:                 English
FAMILY ACC. NUM. COUNT:   47
PATENT INFORMATION:

     PATENT NO.          KIND   DATE       APPLICATION NO.        DATE
     ---------------     ----   --------   --------------------   --------
     US 2005042630        A1    20050224   US 2004-816357         20040401
     US 2004014059        A1    20040122   US 2002-268730         20021009
     US 2005191637        A1    20050901   US 2004-803737         20040318
     US 2005196762        A1    20050908   US 2004-803759         20040318
     US 2005196763        A1    20050908   US 2004-803857         20040318
     US 2005196764        A1    20050908   US 2004-803858         20040318
     US 2005208505        A1    20050922   US 2004-803648         20040318
     US 2005042630        A1    20050224   US 2004-816357         20040401
PRIORITY APPLN. INFO.:                     US 1999-115125P     P  19990106
                                           US 2000-477148      B1 20000104
                                           US 2002-268730      A2 20021009
                                           US 2003-601518      A2 20030620
                                           US 2004-802875      A2 20040312
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                                        US 2004-816357      A  20040401
AB       The present invention is directed to detection and measurement of gene transcripts and
         their equivalent nucleic acid products in blood.  Specifically provided is anal. performed
         on a drop of blood for detecting, diagnosing, and monitoring diseases, and in particular
         asthma, using gene-specific and/or tissue-specific primers.  Affymetrix Human Genome U133
         and ChondroChip microarrays were used to detect differentially expressed gene transcripts
         in hypertension, obesity, allergy, systemic steroids, coronary artery disease, diabetes
         type 2, hyperlipidemia, lung disease, bladder cancer, rheumatoid arthritis,
         osteoarthritis, liver cancer, schizophrenia, Chagas disease, asthma, and manic depression
         syndrome.  The present invention describes methods by which delineation of the sequence
         and/or quantitation of the expression levels of disease-specific genes allows for an
         immediate and accurate diagnostic/prognostic test for disease or to assess the effect of a
         particular treatment regimen.  [This abstract record is one of three records for this
         document necessitated by the large number of index entries required to fully index the
         docoment and publication system constraints.].



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YOU HAVE REQUESTED DATA FROM 3 ANSWERS - CONTINUE? Y/(N):y

L44  ANSWER 2 OF 4      MEDLINE on STN
ACCESSION NUMBER:       2005256428     MEDLINE Full-text
DOCUMENT NUMBER:        PubMed ID: 15809306
TITLE:                  Structural and kinetic analysis of the substrate
                        specificity of human fibroblast
                        activation protein alpha.
AUTHOR:                 Aertgeerts Kathleen; Levin Irena; Shi Lihong; Snell Gyorgy
                        P; Jennings Andy; Prasad G Sridhar; Zhang Yanming; Kraus
                        Michelle L; Salakian Shant; Sridhar Vandana; Wijnands
                        Robert; Tennant Mike G
CORPORATE SOURCE:       Takeda San Diego, Inc., California 92121, USA..
                        kaertgeerts@takedasd.com
SOURCE:                 Journal of biological chemistry, (2005 May 20) 280 (20)
                        19441-4.  Electronic Publication: 2005-04-04.
                        Journal code: 2985121R. ISSN: 0021-9258.
PUB. COUNTRY:           United States
DOCUMENT TYPE:          Journal; Article; (JOURNAL ARTICLE)
LANGUAGE:               English
FILE SEGMENT:           Priority Journals
OTHER SOURCE:           PDB-1Z68
ENTRY MONTH:            200507
ENTRY DATE:             Entered STN: 20050518
                        Last Updated on STN: 20050709
                        Entered Medline: 20050708
AB       Fibroblast activation protein alpha (FAPalpha) is highly expressed in epithelial cancers
         and has been implicated in extracellular matrix remodeling, tumor growth, and metastasis.
         We present the first high resolution structure for the apoenzyme as well as kinetic data
         toward small dipeptide substrates. FAPalpha exhibits a dipeptidyl peptidase IV (DPPIV)-
         like fold, featuring an alpha/beta-hydrolase domain and an eight-bladed beta-propeller
         domain. Known DPPIV dipeptides are cleaved by FAPalpha with an approximately 100-fold
         decrease in catalytic efficiency compared with DPPIV.  Moreover, FAPalpha, but not DPPIV,
         possesses endopeptidase activity toward N-terminal benzyloxycarbonyl (Z)-blocked peptides.
         Comparison of the crystal structures of FAPalpha and DPPIV revealed one major difference
         in the vicinity of the Glu motif (Glu(203)-Glu(204) for FAPalpha; Glu(205)-Glu(206) for
         DPPIV) within the active site of the enzyme. Ala(657) in FAPalpha, instead of Asp(663) as
         in DP-PIV, reduces the acidity in this pocket, and this change could explain the lower
         affinity for N-terminal amines by FAPalpha.  This hypothesis was tested by kinetic
         analysis of the mutant FAPalpha/A657D, which shows on average an approximately 60-fold
         increase in the catalytic efficiency, as measured by k(cat)/K(m), for the cleavage of
         dipeptide substrates.  Furthermore, the catalytic efficiency of the mutant is reduced by
         approximately 350-fold for cleavage of Z-Gly-Pro-7-amino-4-methylcoumarin.  Our data
         provide a clear understanding of the molecular determinants responsible for the substrate
         specificity and endopeptidase activity of FAPalpha.


L44  ANSWER 3 OF 4  CAPLUS  COPYRIGHT 2006 ACS on STN
ACCESSION NUMBER:         2004:964911  CAPLUS Full-text
DOCUMENT NUMBER:          141:389920
TITLE:                    Systems and methods for characterizing a biological
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                         condition or agent using calibrated gene expression
                         profiles
INVENTOR(S):             Bevilacqua, Michael P.; Cheronis, John C.; Tryon,
                         Victor; Bankaitis-Davis, Danute M.
PATENT ASSIGNEE(S):      USA
SOURCE:                  U.S. Pat. Appl. Publ., 90 pp., Cont.-in-part of U.S.
                         Ser. No. 821,850.
                         CODEN: USXXCO
DOCUMENT TYPE:           Patent
LANGUAGE:                English
FAMILY ACC. NUM. COUNT:  7
PATENT INFORMATION:

     PATENT NO.          KIND    DATE          APPLICATION NO.          DATE
     ---------------     ----    --------      --------------------     --------
     US 2004225449        A1     20041111      US 2004-781558           20040217
     US 2003229455        A1     20031211      US 2001-821850           20010329
     US 6692916           B2     20040217
PRIORITY APPLN. INFO.:                         US 1999-141542P      P   19990628
                                               US 2000-195522P      P   20000407
                                               US 2000-605581       B2  20000628
                                               US 2001-821850       A2  20010329
AB     Methods are provided for evaluating a biol. condition of a subject using a calibrated
       profile data set derived from a data set having a plurality of members, each member being
       a quant. measure of the amount of a subject's RNA or protein as distinct constituents in a
       panel of constituents.  The biol. condition may be a naturally occurring physiol. state or
       may be responsive to treatment of the subject with one or more agents.  Calibrated profile
       data sets may be used as a descriptive record for an agent.  The index was determined with
       resp. to a relevant population which has in common property that is at least one of age
       group, gender, ethnicity, geog. location, diet,medical disorder, clin. indicator,
       medication, phys. activity, body mass, and environmental exposure.  The biol. conditions
       include inflammation, diabetes, prostate health or disease, manifested skin, liver
       metabolism and disease, vascular disease, abnormal cell development, cancer and infectious
       disease.  The method can be used for evaluating the effect on a biol. condition by drugs.


L44  ANSWER 4 OF 4  CAPLUS  COPYRIGHT 2006 ACS on STN
ACCESSION NUMBER:        2003:377082  CAPLUS Full-text
DOCUMENT NUMBER:         138:380512
TITLE:                   Systems and methods for characterizing a biological
                         condition or agent using calibrated gene expression
                         profiles
INVENTOR(S):             Bevilacqua, Michael; Cheronis, John C.; Tryon, Victor
PATENT ASSIGNEE(S):      Source Precision Medicine, Inc., USA
SOURCE:                  PCT Int. Appl., 156 pp.
                         CODEN: PIXXD2
DOCUMENT TYPE:           Patent
LANGUAGE:                English
FAMILY ACC. NUM. COUNT:  7
PATENT INFORMATION:

     PATENT NO.          KIND    DATE          APPLICATION NO.          DATE
     ---------------     ----    --------      --------------------     --------
     WO 2003040404        A1     20030515      WO 2002-US36084          20021108
         W:  AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN,
             CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH,
             GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR,
             LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH,
             PL, PT, RO, RU, SC, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT,
             TZ, UA, UG, UZ, VC, VN, YU, ZA, ZM, ZW
         RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, BG,
             CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL,
             PT, SE, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR,
             NE, SN, TD, TG
     CA 2466502           AA     20030515      CA 2002-2466502          20021108
     US 2003219771        A1     20031127      US 2002-291856           20021108
     US 6964850           B2     20051115
     EP 1451340           A1     20040901      EP 2002-792239           20021108
         R:  AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT,
             IE, SI, LT, LV, FI, RO, MK, CY, AL, TR, BG, CZ, EE, SK
     JP 2005508505        T2     20050331      JP 2003-542649           20021108
     US 2005287576        A1    20051229   US 2005-158504         20050622
PRIORITY APPLN. INFO.:                     US 2001-348213P     P  20011109
                                           US 2001-340881P     P  20011207
                                           US 2002-369633P     P  20020403
                                           US 2002-376997P     P  20020430
                                           US 2002-291856      A1 20021108
                                           WO 2002-US36084     W  20021108
AB      A method provides an index that is indicative of the state of a subject, as to a biol.
        condition, based on a sample from the subject.  An embodiment of this method includes:
        deriving from the sample a profile data set, the profile data set including a plurality of
        members, each member being a quant. measure of the amount of a distinct RNA or protein
        constituent in a panel of constituents selected so that measurement of the constituents
        enables evaluation of the biol. condition; and in deriving the profile data set, achieving
        such measure for each constituent under measurement conditions that are substantially
        repeatable; and applying values from the profile data set to an index function that
        provides a mapping from an instance of a profile data set into a single-valued measure of
        biol. condition, so as to produce an index pertinent to the biol. condition of the
        subject.  The index was determined with resp. to a relevant population which has in common
        property that is at least one of age group, gender, ethnicity, geog. location,
        diet,medical disorder, clin. indicator, medication, phys. activity, body mass, and
        environmental exposure.  The biol. conditions include inflammation, diabetes, prostate
        health or disease, manifested skin, liver metabolism and disease, vascular disease,
        abnormal cell development, cancer and infectious disease.  The method can be used for
        evaluating the effect on a biol. condition by drugs.
REFERENCE COUNT:         8     THERE ARE 8 CITED REFERENCES AVAILABLE FOR THIS
                               RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

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